

**WEST**[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)**Search Results -**

Terms	Documents
13 same (conjugat\$ or fuse\$)	10

Database:

US Patents Full-Text Database  
US Pre-Grant Publication Full-Text Database  
JPO Abstracts Database  
EPO Abstracts Database  
Derwent World Patents Index  
IBM Technical Disclosure Bulletins

Refine Search:

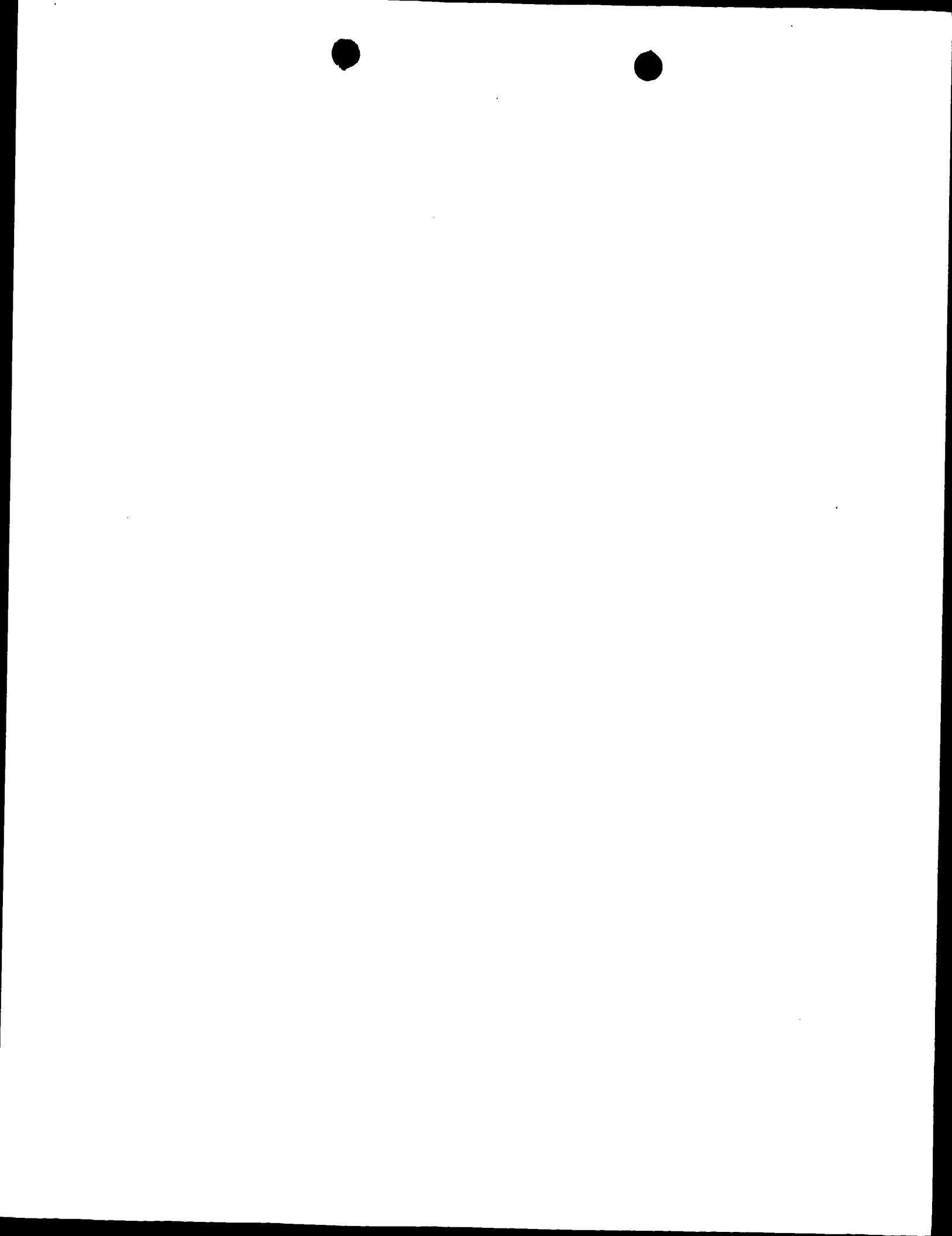
13 same (conjugat\$ or fuse\$)

[Clear](#)**Search History**

Today's Date: 1/17/2002

<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
USPT	13 same (conjugat\$ or fuse\$)	10	<u>L4</u>
USPT	12 same peptide\$	66	<u>L3</u>
USPT	albumin\$ same composition\$ same (stability or stable)	548	<u>L2</u>
USPT	fusion adj (protein\$ or polypeptide\$ or polyprotein\$)	12092	<u>L1</u>

09/424,080



(FILE 'HOME' ENTERED AT 50:47 ON 17 JAN 2002)

FILE 'MEDLINE' ENTERED AT 12:50:55 ON 17 JAN 2002  
L1 128 S ALBUMIN (P) (STABILITY OR STABLE) (P) PEPTIDE?  
L2 20 S L1 AND (FUSION? OR CONJUGATE?)  
L3 20 DUP REM L2 (0 DUPLICATES REMOVED)

=>

09/424,080

1/17/02.



=> d his

(FILE 'HOME' ENTERED AT 13:45:18 ON 17 JAN 2002)  
SET COST OFF

L1 FILE 'REGISTRY' ENTERED AT 13:45:27 ON 17 JAN 2002  
138 S LTEKKYSP/SQSP  
L2 1 S L1 AND 8/SQL

L3 FILE 'HCAOLD' ENTERED AT 13:45:45 ON 17 JAN 2002  
0 S L2

L4 FILE 'HCAPLUS' ENTERED AT 13:45:48 ON 17 JAN 2002  
1 S L2

L5 FILE 'USPATFULL, USPAT2' ENTERED AT 13:46:04 ON 17 JAN 2002  
0 S L2

=> fil reg

FILE 'REGISTRY' ENTERED AT 13:46:19 ON 17 JAN 2002  
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STRUCTURE FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9  
DICTIONARY FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES  
for more information. See STNote 27, Searching Properties in the CAS  
Registry File, for complete details:  
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d l2 sqide can

L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS  
RN 216579-39-4 REGISTRY  
CN L-Proline, L-leucyl-L-threonyl-L-.alpha.-glutamyl-L-lysyl-L-lysyl-L-  
tyrosyl-L-seryl- (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE; STEREOSEARCH  
SQL 8

SEQ 1 LTEKKYSP  
=====

HITS AT: 1-8

MF C44 H72 N10 O14

SR CA

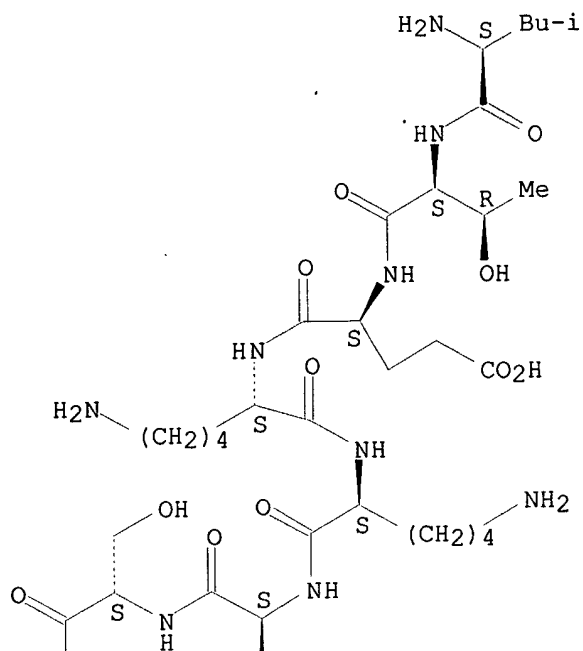
LC STN Files: CA, CAPLUS, TOXCENTER, TOXLIT

Absolute stereochemistry.

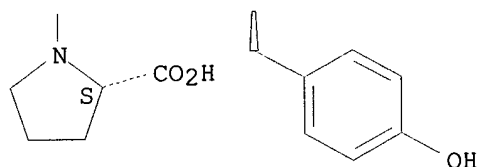
Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
[jan.delaval@uspto.gov](mailto:jan.delaval@uspto.gov)



PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1967 TO DATE)  
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 13:46:26 ON 17 JAN 2002

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FILE COVERS 1907 - 17 Jan 2002 VOL 136 ISS 3

FILE LAST UPDATED: 16 Jan 2002 (20020116/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of





all substance data from the REGISTRY file. Enter HELP FIRST for more information.

HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

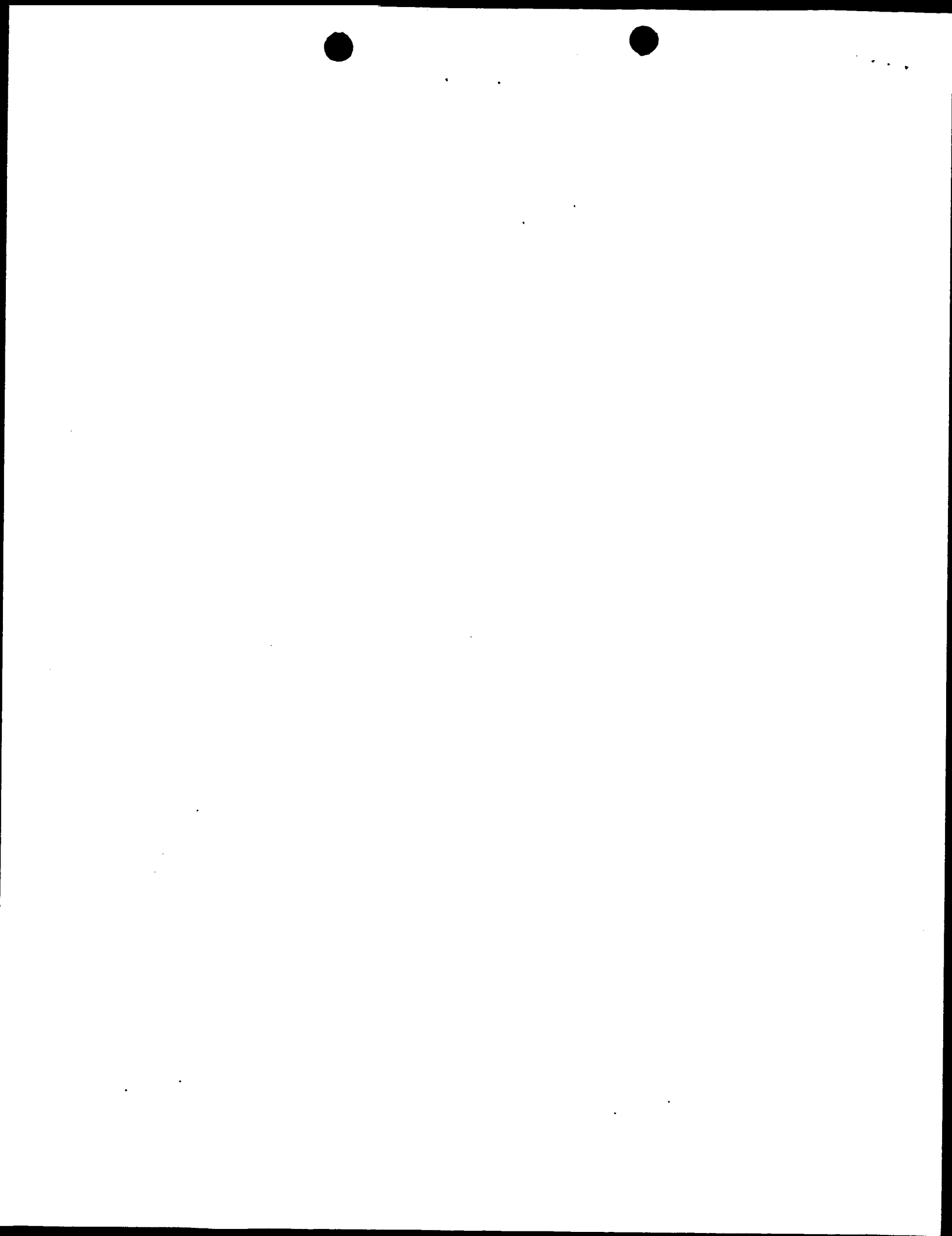
=> d 14 all

L4 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS  
 AN 1998:789037 HCAPLUS  
 DN 130:33014  
 TI Compositions for enhancing immunosuppressants pharmaceutical activities  
 IN Zavialov, Vladimir Petrovich; Vasilenko, Raisa Nikolaevna; Dolgikh, Dmitry Aleksandrovich; Kirpichnikov, Mikhail Petrovich; Navolotskaya, Elena Vitalievna; Korpela, Timo Kalevi  
 PA Russia  
 SO PCT Int. Appl., 26 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 IC ICM A61K038-04  
 ICS A61K038-13; A61K038-21  
 CC 1-7 (Pharmacology)  
 Section cross-reference(s): 15  
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9852594	A1	19981126	WO 1998-FI418	19980518
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
FI 9702121	A	19981120	FI 1997-2121	19970519
AU 9874352	A1	19981211	AU 1998-74352	19980518
EP 981359	A1	20000301	EP 1998-921528	19980518
R: AT, DE, ES, FR, GB, IT, SE, FI				
JP 2001526675	T2	20011218	JP 1998-550009	19980518
PRAI FI 1997-2121	A	19970519		
WO 1998-FI418	W	19980518		
AB	The present invention provides compns. for efficient amplification of immunosuppressive activity of cyclosporins, FK506 or rapamycin to decrease therapeutical dose of immunosuppressants and, as a consequence, avoidance of their undesirable side effects during organ and tissue transplantation, and treatment of different diseases. These compns. include cyclosporins, FK506 or rapamycin and biol. active peptides corresponding to the high-affinity binding/anti-lymphoproliferative site of IFNs-a,b,w,t, or recombinant proteins having the amino acid sequences corresponding to the said site.			
ST	immunosuppressant adjuvant formulation peptide			
IT	Interferon .tau. Interferon .alpha. Interferon .beta.			
RL:	PRP (Properties) (antilymphoproliferative site of; compns. for enhancing			



- immunosuppressant pharmaceutical activities)
- IT Adenocarcinoma inhibitors  
Anti-inflammatory drugs  
Antirheumatic drugs  
Autoimmune diseases  
Drug bioavailability  
Immunosuppressants  
Leukemia inhibitors  
Lupus erythematosus  
Lymphoma inhibitors  
Myasthenia gravis  
Psoriasis  
Transplant (organ)  
Uveitis  
(compns. for enhancing immunosuppressant pharmaceutical activities)
- IT Interferon .alpha.2  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
(compns. for enhancing immunosuppressant pharmaceutical activities)
- IT Peptides, biological studies  
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)  
(compns. for enhancing immunosuppressant pharmaceutical activities)
- IT Interferons  
RL: PRP (Properties)  
(interferon .omega., antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)
- IT Antitumor agents  
(myeloma; compns. for enhancing immunosuppressant pharmaceutical activities)
- IT 216579-39-4D, analogs 216579-44-1D, analogs  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
(compns. for enhancing immunosuppressant pharmaceutical activities)
- IT 53123-88-9, Rapamycin 79217-60-0D, Cyclosporin, derivs. 104987-11-3, Fk506  
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)  
(compns. for enhancing immunosuppressant pharmaceutical activities)
- RE.CNT 5  
RE  
(1) University of Florida; WO 9009806 A2 1990 HCAPLUS  
(2) University of Florida; WO 9410313 A2 1994 HCAPLUS  
(3) Vacsyn, S; FR 2706772 A1 1994 HCAPLUS  
(4) Zarogoulidis, K; Lung Cancer 1996, V15(2), P197 MEDLINE  
(5) Zav'Yalov, V; Mol Immunol 1995, V32(6), P425 HCAPLUS



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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:35 ; Search time 12.72 seconds

(without alignments)  
47.909 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTERKYS P 8

Scoring table: - BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR6:  
2: PIR1:  
3: PIR2:  
4: PIR3:  
5: PIR4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	50.0	8	2	S21663	neuropeptide - flo
2	18	42.9	8	2	S11556	hydrogensulfite re
3	18	42.9	8	2	S15422	adipokinetic hormo
4	18	42.9	8	2	A58641	adipokinetic hormo
5	17	40.5	8	2	A05169	neuropeptide M-I -
6	16	38.1	5	2	G37196	bradykinin-potentl
7	16	38.1	6	2	B44510	hypothetical prote
8	16	38.1	8	2	S20162	leghemoglobin III
9	16	38.1	8	2	A14683	aspartate transam
10	16	38.1	8	2	S45651	prolabe Na+-trans
11	14	33.3	5	1	H0R0HA	proctolin - Americ
12	14	33.3	5	2	A60411	proctolin - Aclant
13	14	33.3	7	2	PT0087	ribulose-bisphosph
14	14	33.3	7	2	S09027	carboxylesterase (
15	14	33.3	7	2	PD0029	pev-kinin 1 - pena
16	14	33.3	8	2	A61348	red pigment-concen
17	14	33.3	8	2	S08995	hypertrehalosemic
18	14	33.3	8	2	A49823	adipokinetic hormo
19	14	33.3	8	2	A44960	neuropeptide Led-C
20	14	33.3	8	2	A43976	hypertrehalosemic
21	14	33.3	8	2	B43976	hypertrehalosemic
22	14	33.3	8	2	S11545	adipokinetic hormo
23	14	33.3	8	2	D47393	neuropeptide calla
24	13	31.0	7	2	PN0150	omega-glucanase I
25	12	28.6	5	2	PQ0689	photosystem I 10.4
26	12	28.6	7	2	S17976	glucose isomerase
27	12	28.6	8	2	S16324	hypothetical prote
28	12	28.6	8	2	A23967	leucopyrokinin - M
29	11	26.2	4	2	E44823	synaptosomal-assoc

30	11	26.2	5	2	A41225	copper resistance
31	11	26.2	5	2	D60274	major protein anti
32	11	26.2	5	2	PT0714	T-cell receptor be
33	11	26.2	6	2	A61411	ameletin - rat
34	11	26.2	6	2	A44916	mosquitoicidal tox
35	11	26.2	6	2	A27696	contraction-inhibi
36	11	26.2	6	2	PT0618	T-cell receptor be
37	11	26.2	6	2	PT0715	T-cell receptor be
38	11	26.2	6	2	I49421	laminin BI - weste
39	11	26.2	7	2	A60139	fatty-acid synthas
40	11	26.2	7	2	E30608	ig kappa chain V-I
41	11	26.2	7	2	S42620	agrecan - bovine
42	11	26.2	7	2	I48086	DNA topoisomerase
43	11	26.2	7	2	PH0932	T-cell receptor de
44	11	26.2	7	4	A58725	virotloxin - destro
45	11	26.2	8	2	S08996	hypertrehalosemic

#### ALIGNMENTS

RESULT 1  
S21663  
neuropeptide - flower beetle (Pachnoda marginata)  
C:Species: Pachnoda marginata  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S21663  
R:Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992  
A:Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va  
electrometry.  
A:Reference number: S21663; MUID:92265187  
A:Accession: S21663  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <GAE>

Query Match 50.0%; Score 21; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
DB 1 ELNYS P 6

RESULT 2  
S11556  
hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragmen  
N:Alternate names: bisulfite reductase; desulfotuscidin  
C:Species: Desulfovibrio thermophilus  
C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C:Accession: S11556  
R:Paugue, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.J.G.  
Biochim. Biophys. Acta 1040, 112-118, 1990  
A:Title: Purification and characterization of bisulfite reductase (desulfotuscidin) f  
A:Reference number: S11024; MUID:90335276  
A:Accession: S11556  
A:Molecule type: protein  
A:Residues: 1-6 <FAU>  
C:Keywords: oxidoreductase

Query Match 42.9%; Score 18; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKY 6  
DB 1:11  
2 EKKY 5

## RESULT 3

S15422

adipokinetin hormone - cockchafer

C:Species: Melolontha melolontha (cockchafer)

C:Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997

C:Accession: S15422

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A:Title: A unique charged tyrosine-containing member of the adipokinetin hormone/ red-pi

A:Reference number: S15422; MUID:91248100

A:Accession: S15422

A:Molecule type: protein

A:Residues: 1-8 &lt;BIO&gt;

C:Superfamily: adipokinetin hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 42.9%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8

DB 4 YSP 6

## RESULT 4

A58641

adipokinetin hormone - dor beetle

C:Species: Geotrupes stercoratus (dor beetle)

C:Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997

C:Accession: A58641

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A:Title: A unique charged tyrosine-containing member of the adipokinetin hormone/ red-pi

A:Reference number: S15422; MUID:91248100

A:Accession: A58641

A:Molecule type: protein

A:Residues: 1-8 &lt;BIO&gt;

C:Superfamily: adipokinetin hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 42.9%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8

DB 4 YSP 6

## RESULT 5

A05169

neuropeptide M-1 - American cockroach

C:Species: Periplaneta americana (American cockroach)

C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Dec-1993

C:Accession: A05169

R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas

A:Reference number: A90118; MUID:85046550

A:Accession: A05169

A:Molecule type: protein

A:Residues: 1-8 &lt;WTP&gt;

C:Keywords: neuropeptide

Query Match

Best Local Similarity 40.5%; Score 17; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8

DB 1 EVNESP 6

## RESULT 6

G37196

bradykinin-potentiating peptide 7 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C:Accession: G37196

R:Chitra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptide

A:Reference number: A37196; MUID:90351557

A:Accession: G37196

A:Molecule type: protein

A:Residues: 1-5 &lt;CTN&gt;

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 38.1%; Score 16; DB 2; Length 5;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKYSF 8

DB 1 QKNAP 5

## RESULT 7

B44510

hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)

C:Species: Lactococcus lactis

C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 30-Sep-1993

C:Accession: B44510

R:Renault, P.; Gallard, C.; Heslot, H.

J. Bacteriol. 171, 3108-3114, 1989

A:Title: Product of the Lactococcus lactis gene required for malolactic fermentation

A:Reference number: A44510; MUID:89255069

A:Accession: B44510

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 &lt;REN&gt;

A:Cross-references: EMBL:M90762

Query Match

Best Local Similarity 38.1%; Score 16; DB 2; Length 6;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKKYF 6

DB 2 EKKYF 5

## RESULT 8

S20162

leghemoglobin III - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 04-Mar-2000

C:Accession: S20162

R:Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.

Mol. Gen. Genet. 214, 181-191, 1988

A:Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-n

A:Reference number: S08322; MUID:89181515

A:Accession: S20162

A:Molecule type: DNA

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:15:20 ; Search time 10.03 Seconds  
(without alignments)  
29.244 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42  
Sequence: 1 LTRKXSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	45.2	8	1	OH09_RAT
2	18	42.9	8	1	AKH_MELML
3	16	38.1	5	1	BPP7_BOTIN
4	14	33.3	5	1	PRCT_PERAM
5	14	33.3	6	1	ASP2_LACSN
6	14	33.3	6	1	OWM_LBPDE
7	14	33.3	8	1	ALL4_CAIYO
8	14	33.3	8	1	HTFL_PERAM
9	14	33.3	8	1	HTFL_TENMO
10	14	33.3	8	1	RPCH_PANBO
11	13	31.0	8	1	LMT2_LOCM1
12	12	28.6	7	1	AL17_CYDPO
13	12	28.6	8	1	AL13_CYDPO
14	12	28.6	8	1	AL14_CYDPO
15	12	28.6	8	1	AL14_CYDPO
16	12	28.6	8	1	LPK_LEUMA
17	11	26.2	5	1	AL14_CARMA
18	11	26.2	6	1	CIP1_MYTED
19	11	26.2	7	1	VP19_HSVIK
20	11	26.2	7	1	AL17_CYDPO
21	11	26.2	8	1	AKH_TIRAU
22	11	26.2	8	1	AKH_TIRAU
23	11	26.2	8	1	AKH_TIRAU
24	11	26.2	8	1	AL15_CARMA
25	11	26.2	8	1	AL18_CARMA
26	11	26.2	8	1	AL17_CYDPO
27	11	26.2	8	1	AL17_CYDPO
28	11	26.2	8	1	HTF2_PERAM
29	11	26.2	8	1	LCR8_LEUMA
30	11	26.2	8	1	PPK2_PERAM
31	10	23.8	7	1	IGAO_DACDE
32	10	23.8	8	1	FAR4_HOMAM
33	10	23.8	8	1	NPB_BOVIN

34	9	21.4	5	1	FARP_ARTTR
35	9	21.4	7	1	MSCL_SALTY
36	9	21.4	7	1	UC24_MALZE
37	9	21.4	7	1	WMA2_ACHPU
38	9	21.4	7	1	WMA3_ACHPU
39	9	21.4	8	1	ACT_THUAL
40	9	21.4	8	1	ANG2_BORTA
41	9	21.4	8	1	B4AK_FORST
42	9	21.4	8	1	UPAA_HUMAN
43	8	19.0	4	1	RM01_YEAST
44	8	19.0	5	1	PAV2_PARMA
45	8	19.0	5	1	PSK_DAUCA

## ALIGNMENTS

RESULT 1  
ID OH09\_RAT STANDARD: PRT: 8 AA.  
AC P56575;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=WISTAR; TISSUE=Heart;  
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
RA Jungblut P.R.;  
RL Submitted (SEP-1998) TO THE SWISS-PROT data bank.  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 8.9, ITS MW IS: 42 KDA.  
FT NON-TER  
SQ SEQUENCE 8 AA: 1029 MW: 9E0775A6CA140B06 CRC64;

Query Match 45.2% Score 19; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1e+05; 1; Indels 0; Gaps 0;  
Matches 3; Conservative 2; Mismatches 1;  
QY 3 EKKYSP 8  
DB 2 ERKOSP 7  
RESULT 2  
ID AKH\_MELML STANDARD: PRT: 8 AA.  
AC P25423;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE ADIPOKINETIC HORMONE (AKH).  
OS Melolontha melolontha (Cockchafer),  
OS Geotrupes stercorosus (Dor beetle), and  
OS Pterodroma marginata (Pterodroma);  
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.  
OX NCBI\_TaxID=7061, 7087, 7058;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;  
RX MEDLINE=91248100; Pubmed=2039445;  
RA Gaede G.;  
RT "A unique charged tyrosine-containing member of the adipokinetin  
hormone/red-pigment-concentrating hormone peptide family isolated and  
sequenced from two beetle species.";

RL Biochem. J. 275:671-677(1991).  
 RN (2)  
 RP SEQUENCE.  
 RC SPECIES-P. marginata; TISSUE-Corpora cardiaca;  
 RX MEDLINE-9226518; Pubmed-1586453;  
 RA Gade G., Lopata A., Kellner R., Rinehart K.L. Jr.;  
 RT "Primary structures of neuropeptides isolated from the corpora  
 cardiaca of various cetoid beetle species determined by  
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass  
 RT spectrometry."  
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).  
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.  
 CC PIR: S15422; S15422.  
 CC PIR: S21663; S21663.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00295; AKH; 1.  
 KM Neuropeptide; Amidation; Flight.  
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD.RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1022 MW; 867AB75AB544736 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 YSP 8  
 1 1  
 Db 4 YSP 6

RESULT 3  
 ID BPT7\_BOTIN STANDARD; PRT; 5 AA.  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE BRADYKININ-POTENTIATING PEPTIDE S5.2 (5A) (ANGIOTENSIN-CONVERTING  
 DE ENZYME INHIBITOR).  
 OS Bothrops insularis (Island jararaca) (Oueimada jararaca).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 CC Viperidae; Crotalinae; Bothrops.  
 NC NCB1\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Venom;  
 RX MEDLINE-90351557; Pubmed-2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE  
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF  
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.  
 DR PIR: G37196; G37196.  
 KM Hypotensive agent; Venom.  
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B0000 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 5;  
 Best Local Similarity 40.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 OKMAP 5

RESULT 4  
 ID PRC2\_PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE PROCTOLIN.  
 OS Periplaneta americana (American cockroach),  
 OS Limulus polyphemus (Atlantic horseshoe crab), and  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Plekoptera; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 CC Blattodea; Blattella; Periplaneta.  
 CC NCB1\_TaxID=6978; 6850, 6759;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES-P.americana;  
 RX MEDLINE-76074708; Pubmed-576;  
 RA Starratt A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 RT in insects."  
 RL Life Sci. 17:1253-1256(1975).  
 RN [2]  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES-P.americana;  
 RX MEDLINE-81225865; Pubmed-6113690;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron."  
 RL Science 213:567-569(1981).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES-L.polyphemus;  
 RX MEDLINE-90287800; Pubmed-2356151;  
 RA Groome J.R., Tillinghast E.K., Townley M.A., Velours A.,  
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus."  
 RL Peptides 11:205-211(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES-C.maenas;  
 RX MEDLINE-86232789; Pubmed-2872661;  
 RA Stangier J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 RT pericardial organs of the shore crab, Carcinus maenas."  
 RL Peptides 7:67-72(1986).  
 CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
 CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 CC PIR: A01644; HOROHA.  
 DR PIR: A60411; A60411.  
 KM Neuropeptide.  
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 33.3%; Score 14; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KYSP 8  
 1 1  
 Db 1 KYLP 4

RESULT 5  
 ID ASP2\_LACSN STANDARD; PRT; 6 AA.  
 ID ASP2\_LACSN



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:50 ; Search time 22.03 Seconds  
(without alignments)  
53.118 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTKKYSR 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	59.5	8	2 Q9R9E0	Q9R9E0 bacillus su
2	14	33.3	7	13 P82101	P82101 litorea rub
3	14	33.3	8	8 Q9TMM4	Q9TMM4 begonia for
4	14	33.3	8	8 Q9TMY2	Q9TMY2 begonia tai
5	14	33.3	8	8 Q9TXY1	Q9TXY1 begonia apt
6	14	33.3	8	10 Q9XGL9	Q9XGL9 begonia nan
7	14	33.3	8	10 Q9XGL8	Q9XGL8 begonia chi
8	14	33.3	8	10 Q9XGL8	Q9XGL8 begonia pal
9	13	31.0	8	12 Q9R7T2	Q9R7T2 escherichia
10	13	31.0	8	12 Q9R7T2	Q9R7T2 human papil
11	12	28.6	8	6 Q9XSY1	Q9XSY1 canis famill
12	12	28.6	8	8 Q35792	Q35792 saccharomyc
13	12	28.6	8	11 Q62933	Q62933 rattus norv
14	12	26.2	7	2 Q54248	Q54248 streptomyce
15	11	26.2	8	2 Q56429	Q56429 thermus aqu
16	11	26.2	8	2 Q9R5L7	Q9R5L7 clostridium
17	11	26.2	8	4 Q15895	Q15895 homo sapien
18	11	26.2	8	5 P82689	P82689 periplaneta
19	11	26.2	8	6 P82929	P82929 bos taurus

20	11	26.2	8	6 Q9BFA7	Q9BFA7 macrocellid
21	11	26.2	8	7 Q95213	Q95213 oryctolagus
22	11	26.2	8	8 Q9TXY3	Q9TXY3 begonia for
23	10	23.8	6	10 P82541	P82541 psathia o1
24	10	23.8	7	8 P92385	P92385 psathia o1
25	10	23.8	7	8 P92385	P92385 psathia o1
26	10	23.8	7	8 P92210	P92210 hordeum mar
27	10	23.8	7	8 P92214	P92214 hordeum mar
28	10	23.8	7	8 P92214	P92214 hordeum mar
29	10	23.8	7	8 P92221	P92221 bromus iner
30	10	23.8	7	8 P92226	P92226 crithopsis
31	10	23.8	7	8 P92372	P92372 haynaldia v
32	10	23.8	7	8 P92381	P92381 hordeum bra
33	10	23.8	7	8 P92387	P92387 henrardia p
34	10	23.8	7	8 P92390	P92390 henrardiel
35	10	23.8	7	8 P92393	P92393 hordeum vul
36	10	23.8	7	8 P92425	P92425 pseudoroegn
37	10	23.8	7	8 P92427	P92427 peridictyon
38	10	23.8	7	8 P92430	P92430 aegilops ta
39	10	23.8	7	8 P92440	P92440 taenialtheru
40	10	23.8	7	8 P92442	P92442 thnopyrum
41	10	23.8	7	8 P92403	P92403 thnopyrum
42	10	23.8	7	12 Q66205	Q66205 porcine tra
43	10	23.8	8	2 Q44463	Q44463 agrobacteri
44	10	23.8	8	2 Q92IE9	Q92IE9 neisseria m
45	10	23.8	8	2 Q9R5R0	Q9R5R0 shigella dy

## ALIGNMENTS

RESULT 1  
ID Q9R9E0 PRELIMINARY: PRT: 8 AA.  
AC Q9R9E0:  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-MAY-2000 (TREMREL. 13, Last annotation update)  
DE STAGE V SPORULATION PROTEIN E (FRAGMENT).  
GN SPOVE.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP STRAIN=168;  
RC MEDLINE=93003529; PubMed=1391053;  
RX Henriques A.O., de Lencastre H., Pigot P.J.;  
RA "A Bacillus subtilis morphogene cluster that includes spve is  
RT homologous to the mra region of Escherichia coli.";  
RL Biochimie 74:735-748(1992).  
DR EMBL; X64258; CAA43556.1; -.  
FT NON-TER  
SQ SEQUENCE 8 AA: 893 MW; EE75A1A33321B1A6 CRC64;

Query Match 59.5%; Score 25; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.7e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTKKYSR 8  
: | | | |  
Db 1 MTKTKRSP 8  
RESULT 2  
ID P82101 PRELIMINARY: PRT: 7 AA.  
AC P82101:  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-MAY-2000 (TREMREL. 13, Last annotation update)

DE ELECTRIN 5.  
 OS Litorea rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litorea.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=SKIN SECRETION;  
 RA Mambitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litorea electrica. Comparison with the skin peptides from Litorea  
 RT rubella.";  
 RL Aust. J. Chem. 52:0-0(1999).  
 KW Amphibian skin; Amidation.  
 FT MOD\_RES  
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 33.3%; Score 14; DB 13; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YSP 8  
 Db 2 YEP 4

RESULT 3  
 ID 09TMN4 PRELIMINARY; PRT; 8 AA.  
 AC 09TMN4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE RBCL PROTEIN (FRAGMENT).  
 OS Begonia formosana.  
 OC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Cucurbitales; Begoniaceae; Begonia.  
 OX NCBI\_TaxID=80370;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chiang T.Y.;  
 RT "Sequence announcement: rbcl promoter gene in Begonia formosana."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 EMBL: AJ009397; CAB52119.1;  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 8; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TEKK 5  
 Db 5 TETK 8

RESULT 4  
 ID 09T2Y2 PRELIMINARY; PRT; 8 AA.  
 AC 09T2Y2;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE RBCL PROTEIN (FRAGMENT).  
 GN RBCL.  
 OS Begonia taipeiensis.

OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Cucurbitales; Begoniaceae; Begonia.  
 OX NCBI\_TaxID=80371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chiang T.Y.;  
 RT "Sequence announcement: rbcl promoter gene in Begonia formosana."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 EMBL: AJ009602; CAB52129.1;  
 DR EMBL: AJ009600; CAB52125.1;  
 DR EMBL: AJ009601; CAB52127.1;  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 8; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TEKK 5  
 Db 5 TETK 8

RESULT 5  
 ID 09T2Y1 PRELIMINARY; PRT; 8 AA.  
 AC 09T2Y1;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE RBCL PROTEIN (FRAGMENT).  
 OS Begonia aptera.  
 OC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC eurosids I; Cucurbitales; Begoniaceae; Begonia.  
 OX NCBI\_TaxID=71278;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chiang T.Y.;  
 RT "Sequence announcement: rbcl promoter gene in Begonia formosana."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 EMBL: AJ009603; CAB52086.1;  
 DR EMBL: AJ009604; CAB52080.1;  
 DR EMBL: AJ009605; CAB52084.1;  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 8; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TEKK 5  
 Db 5 TETK 8

RESULT 6  
 ID 09XG19 PRELIMINARY; PRT; 8 AA.  
 AC 09XG19;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DE ATPB PROTEIN (FRAGMENT).



CC The sequence is that of a peptide signal sequence which can be used  
 CC to treat diseases involving human leucocyte interferons, including  
 CC cancer, immunodeficiencies and infectious diseases.  
 CC See also AAB5944-83.

CC Sequence 6 AA;

Query Match 61.9%; Score 26; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EKYS 7  
 |||||  
 Db 2 ekys 6

# RESULT 2

AAB36378  
 ID AAB36378 standard; Peptide: 6 AA.

AC AAB36378;

DT 27-FEB-2001 (first entry)

DE Rat SmlIM/CRP2 putative nuclear localisation signal SEQ ID NO:15.

KM Hypertension; inhibition; treatment; SmlIM; CRP; LIM domain;

XX smooth muscle cell LIM; vascular smooth muscle cell; hypotensive.

OS Rattus sp.

PN WO200066734-A1.

PD 09-NOV-2000.

PF 05-MAY-2000; 2000MO-US12189.

PR 05-MAY-1999; 9905-0305839.

PA (HARD) HARVARD COLLEGE.

PI Lee M, Yet S;

DR WPI; 2000-687540/67.

XX Novel nucleic acid encoding a regulatory sequence which acts  
 PT preferentially in vascular smooth muscle cells, operatively linked to  
 PT an antisense template, used to treat hypertension -

PS Disclosure; Page 33; 91pp; English.

CC The present invention describes a nucleic acid, comprising a sequence  
 CC at least 50 % identical to a mouse SmlIM/CRP promoter cis-acting  
 CC regulatory sequence, operably linked to an antisense template  
 CC complementary to part of an mRNA encoding a vascular smooth muscle cell  
 CC polypeptide. The first sequence directs expression of the second  
 CC preferentially in the first sequence smooth muscle cells. Also described are:  
 CC (1) screening candidate compounds to identify a compound capable of  
 CC decreasing expression of SmlIM/CRP2 in vascular smooth muscle cells,  
 CC comprising: (a) contacting a vascular smooth muscle cell with a  
 CC candidate compound; and (b) determining the amount of SmlIM/CRP2  
 CC expression in the cell; and (2) a transgenic non-human mammal, the  
 CC germ cells and somatic cells of which comprise a null mutation in a  
 CC gene encoding SmlIM. The nucleic acids can be used for identifying  
 CC compounds that decrease expression of SmlIM/CRP2 in vascular smooth  
 CC muscle cells. Compounds that reduce the expression of SmlIM can be  
 CC used to decrease hypertension in mammals. Compounds that reduced SmlIM  
 CC activity can be used to inhibit hypertension in mammals. AAC64704 to  
 CC AAC64723 and AAB36370 to AAB36384 represent sequences used in the  
 CC exemplification of the present invention.

XX Sequence 6 AA;

Query Match 57.1%; Score 24; DB 21; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 KKYS 8  
 |||||  
 Db 1 kkyyp 5

# RESULT 3

AAE05552  
 ID AAE05552 standard; peptide: 6 AA.

AC AAE05552;

DT 24-SEP-2001 (first entry)

DE NLS of rat smooth muscle cell LIM (SmlIM/CRP2) protein.

KM Rat; smooth muscle cell LIM; SmlIM/CRP2 protein; arteriosclerosis;

KM neointima formation; balloon angioplasty; vascular disease; cardiac;

KM angiogenesis; peripheral vascular disease; coronary artery disease;

XX gene therapy; antisense therapy; nuclear localisation signal; NLS.

OS Rattus sp.

PN US6258557-B1.

PD 10-JUL-2001.

PF 14-MAR-1997; 97US-0818655.

PR 15-MAR-1996; 96US-0616368.

PA (HARD) HARVARD COLLEGE.

PI Lee M, Haber E, Jain M, Yet S;

DR WPI; 2001-450366/48.

XX Isolated DNA encoding smooth muscle cell LIM (SmlIM/CRP2) useful for  
 PT inhibiting arterial smooth muscle proliferation and for treating  
 PT peripheral vascular disease, arteriosclerosis and coronary artery  
 PT disease -

PS Disclosure; Column 19; 38pp; English.

CC The invention relates to an isolated DNA which regulates vascular  
 CC smooth muscle cell-specific transcription of a polypeptide-encoding  
 CC sequence to which it is operably linked. The invention is based on  
 CC the identification and characterisation of a smooth muscle cell LIM  
 CC (SmlIM/CRP2) polypeptide which is expressed preferentially in arterial  
 CC smooth muscle cells. SmlIM/CRP2 sequence is useful for directing  
 CC vascular smooth muscle cell-specific expression of a polypeptide, by  
 CC introducing vector comprising SmlIM/CRP2 into a vascular smooth muscle  
 CC cell and maintaining cell under conditions suitable for polypeptide  
 CC expression. SmlIM/CRP2 is useful for inhibiting arterial smooth muscle  
 CC proliferation and for inhibiting neointima formation after balloon  
 CC angioplasty. SmlIM/CRP2 nucleotide sequence is useful for increasing  
 CC the level of SmlIM/CRP2 polypeptide in injured vascular tissues for  
 CC inhibiting proliferation of smooth muscle cells. SmlIM/CRP2 is useful  
 CC in gene therapy and antisense therapy for treating vascular diseases  
 CC such as arteriosclerosis, and to promote angiogenesis to treat diseases  
 CC present sequence is nuclear localisation signal (NLS) of rat smooth  
 CC muscle cell LIM (SmlIM/CRP2) protein.

XX Sequence 6 AA;

Query Match 57.1%; Score 24; DB 22; Length 6;

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:15 ; Search time 12.51 Seconds  
(without alignments)  
14.391 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTERKSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	2	US-08-669-284B-30
2	26	61.9	6	5	PCT-US93-12679-16
3	24	57.1	6	1	US-08-616-368A-15
4	24	57.1	6	4	US-09-054-298-15
5	24	57.1	6	4	US-08-818-655-15
6	24	57.1	6	4	US-08-891-271-13
7	22	52.4	7	3	US-08-756-849-123
8	21	50.0	7	3	US-08-444-818-659
9	20	47.6	7	3	US-08-390-353A-9
10	20	47.6	7	4	US-09-371-710-48
11	20	47.6	7	4	US-09-147-933-31
12	20	47.6	7	4	US-08-862-124-26
13	20	47.6	7	4	US-08-862-124-26
14	20	47.6	7	4	US-09-648-386-48
15	20	47.6	7	4	US-08-178-570-47
16	20	47.6	7	4	US-08-369-643-47
17	20	47.6	7	4	PCT-US95-00147-47
18	20	47.6	7	4	US-08-676-378-8
19	19	45.2	7	1	US-07-638-492-15
20	19	45.2	7	3	US-08-604-965E-10
21	19	45.2	7	3	US-08-604-965E-10
22	19	45.2	7	3	US-08-604-965E-10
23	19	45.2	7	3	US-08-604-965E-10
24	19	45.2	7	3	US-08-604-965E-10
25	19	45.2	7	3	US-08-604-965E-10
26	19	45.2	7	3	US-08-604-965E-10
27	18	42.9	5	2	US-08-928-958-20

28	18	42.9	5	2	US-09-072-429-20	Sequence 20, Appl
29	18	42.9	6	1	US-08-082-847-13	Sequence 13, Appl
30	18	42.9	6	2	US-08-928-958-21	Sequence 21, Appl
31	18	42.9	6	2	US-09-072-429-21	Sequence 21, Appl
32	18	42.9	6	2	US-09-127-574-17	Sequence 17, Appl
33	18	42.9	6	2	US-09-127-574-17	Sequence 70, Appl
34	18	42.9	6	4	US-09-496-379-70	Sequence 10, Appl
35	18	42.9	6	4	US-09-496-379-70	Sequence 11, Appl
36	18	42.9	6	4	US-09-496-379-11	Sequence 11, Appl
37	18	42.9	7	1	US-08-082-847-17	Sequence 25, Appl
38	18	42.9	7	1	US-08-082-847-25	Sequence 1, Appl
39	18	42.9	7	1	US-08-218-027A-2	Sequence 2, Appl
40	18	42.9	7	1	US-08-218-027A-2	Sequence 4, Appl
41	18	42.9	7	1	US-08-218-027A-6	Sequence 6, Appl
42	18	42.9	7	1	US-08-218-027A-6	Sequence 7, Appl
43	18	42.9	7	1	US-08-218-027A-7	Sequence 7, Appl
44	18	42.9	7	1	US-08-040-548-40	Sequence 40, Appl
45	18	42.9	7	1	US-08-466-344-40	Sequence 40, Appl

## ALIGNMENTS

RESULT 1  
US-08-669-284B-30  
Sequence 30, Application US/08669284B  
Patent No. 5939534  
GENERAL INFORMATION:  
APPLICANT: Inoue, Makoto  
APPLICANT: Kikuchi, Kaoru  
APPLICANT: Ishige, Yoko  
APPLICANT: Ito, Akira  
APPLICANT: Kimura, Toru  
APPLICANT: Nakayama, Chikao  
APPLICANT: No. 5939534uchi, Hiroshi  
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUTROTROPIC FACTORS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS: SUGHRUE, MION, ZINN, MACPHEE & SEAS  
ADDRESS: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,284B  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/02269  
FILING DATE: 27-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-268281  
FILING DATE: 05-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-201504  
FILING DATE: 02-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 05-350934  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Dean H.  
REGISTRATION NUMBER: 33,981  
REFERENCE/DOCKET NUMBER: O-42041  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-284B-30

Query Match 100.0%; Score 42; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKISP 8  
Db 1 LTKKISP 8

## RESULT 2

PCT-US93-12679-16  
Sequence 16, Application PC/TUS9312679  
GENERAL INFORMATION:

APPLICANT: Rath, Mathias  
TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO  
TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES - METHODS OF IDENTIFICATION AND  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHELDON S. MARK  
STREET: 401 Florence Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12679  
FILING DATE: 30-DEC-1993  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Cranfill, Raymond B  
REGISTRATION NUMBER: 32,845  
REFERENCE/DOCKET NUMBER: RATH-10016PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5333  
TELEFAX: 415-322-5499  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US93-12679-16

Query Match 61.9%; Score 26; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKS 7  
Db 2 EKKS 6

## RESULT 3

US-08-616-368A-15  
Sequence 15, Application US/08616368A  
Patent No. 5767262  
GENERAL INFORMATION:

APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar  
APPLICANT: Jain, Mukesh  
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,368A  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/022001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-616-368A-15

Query Match 57.1%; Score 24; DB 1; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKXSP 8  
Db 1 KKXSP 5

## RESULT 4

US-09-054-298-15  
Sequence 15, Application US/09054298  
Patent No. 6136953  
GENERAL INFORMATION:

APPLICANT: Lee, Mu-En  
APPLICANT: Haber, Edgar  
APPLICANT: Jain, Mukesh  
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054,298

Query Match 57.1%; Score 24; DB 1; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FILING DATE: 02-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/616,368  
FILING DATE: 15-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ph.D., Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 05433/022002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKYP 8  
1111  
Db 1 KKYP 5

RESULT 5  
US-08-818-655-15  
Sequence 15, Application US/08818655  
Patent No. 6258557

## GENERAL INFORMATION:

APPLICANT: Lee, Mu-En  
APPLICANT: Jain, Mukesh  
APPLICANT: Yet, Shaw-Fang  
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,655  
FILING DATE: 14-MAR-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/616,368  
FILING DATE: 15-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Frieder, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/030001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-818-655-15

Query Match 57.1%; Score 24; DB 4; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKYP 8  
1111  
Db 1 KKYP 5

RESULT 6

US-08-891-271-13  
Sequence 13, Application US/08891271  
Patent No. 6165476

## GENERAL INFORMATION:

APPLICANT: Strom, Terry B.  
APPLICANT: Sytkowski, Arthur J.  
APPLICANT: Zheng, Xia Xiao  
TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin  
TITLE OF INVENTION: Hing Region Linker  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,271  
FILING DATE: 10-JUL-1997  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Hogle, Doreen M.  
REGISTRATION NUMBER: 36,361  
REFERENCE/DOCKET NUMBER: BIH97-07  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540

## INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-891-271-13

Query Match 57.1%; Score 24; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKYP 8  
1111  
Db 1 EKYP 6

RESULT 7

US-08-756-849-123  
Sequence 123, Application US/08756849  
Patent No. 6093810

## GENERAL INFORMATION:

APPLICANT: Bird, David M.  
APPLICANT: Wilson, Mark A.  
TITLE OF INVENTION: Nematode-Induced Genes in Tomato

NUMBER OF SEQUENCES: 129  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,849  
FILING DATE: 26-NOV-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,474  
FILING DATE: 23-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-05351005  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-756-849-123

Query Match 52.4%; Score 22; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEKKISP 8  
DB 1 TSPSYSP 7

RESULT 8  
US-08-444-818-659  
Sequence 959, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
APPLICANT: Butler, William J.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590

FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hardin, Ailsa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 659:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-659

Query Match 50.0%; Score 21; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.6e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERLY 6  
DB 1 LTERLY 6

RESULT 9  
US-08-390-353A-9  
Sequence 9, Application US/08390353A  
Patent No. 6107457  
GENERAL INFORMATION:  
APPLICANT: Arlinghaus, Ralph B.  
APPLICANT: Liu, Jiaxin  
APPLICANT: Lu, Dia  
APPLICANT: Lopez-Berestein, Gabriel  
TITLE OF INVENTION: Bcr-Abl Directed Compositions and Uses for  
TITLE OF INVENTION: Regulating Philadelphia Chromosome Stimulated  
TITLE OF INVENTION: Cell Activity  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,353A  
FILING DATE: 16-FEB-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mayfield, Denise L.  
REGISTRATION NUMBER: 33,732  
REFERENCE/DOCKET NUMBER: US/SC:421/MAY  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
TELLEX: N/A  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-353A-9



Query Match 47.6%; Score 20; DB 3; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 KXSP 8  
: |||  
Db 1 RSYP 5

RESULT 10  
US-09-371-710-48  
; Sequence 48, Application US/09371710A  
; Patent No. 6146868  
; GENERAL INFORMATION:  
; APPLICANT: Kozel, Thomas R.  
; APPLICANT: Bloomer, Sherri L.  
; APPLICANT: Savoy, Anne C.  
; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of  
; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof  
; FILE REFERENCE: D6245  
; CURRENT APPLICATION NUMBER: US/09/371,710A  
; CURRENT FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 50  
; SEQ ID NO 48  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer  
US-09-371-710-48

Query Match 47.6%; Score 20; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 KXSP 8  
: |||  
Db 2 KYAP 5

RESULT 11  
US-09-147-933-31  
; Sequence 31, Application US/09147933A  
; Patent No. 6168917  
; GENERAL INFORMATION:  
; APPLICANT: Kilpatrick, David  
; TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF  
; TITLE OF INVENTION: NON-POLIO ENTEROVIRUSES  
; FILE REFERENCE: 62242/US  
; CURRENT APPLICATION NUMBER: US/09/147,933A  
; CURRENT FILING DATE: 1999-07-09  
; EARLIER APPLICATION NUMBER: PCT/US97/17734  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: U. S. 60/027,353  
; EARLIER FILING DATE: 1996-10-02  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide  
US-09-147-933-31

Query Match 47.6%; Score 20; DB 4; Length 7;  
Best Local Similarity 42.9%; Pred. No. 1.6e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTKKTS 7

Db 1 ITRRYT 7  
: |||

RESULT 12  
US-08-862-124-23  
; Sequence 23, Application US/08862124  
; Patent No. 6207153  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Maiti, Howard A.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
; TITLE OF INVENTION: DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster LLP  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/862,124  
; FILING DATE: 22-MAY-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 31608-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-862-124-23

Query Match 47.6%; Score 20; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 KXSP 8  
: |||  
Db 3 RYSP 6

RESULT 13  
US-08-862-124-26  
; Sequence 26, Application US/08862124  
; Patent No. 6207153  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Maiti, Pradip K.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
; TITLE OF INVENTION: DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-862-124-26

Query Match 47.6%; Score 20; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KYSP 8  
DB 3 KYSP 6

RESULT 14  
US-09-648-386-48  
Sequence 48, Application US/09648386  
Patent No. 6284308  
GENERAL INFORMATION:  
APPLICANT: Kozel, Thomas R.  
APPLICANT: Bloomer, Sherri L.  
APPLICANT: Savoy, Anne C.  
TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of  
FILE REFERENCE: D6245D  
CURRENT APPLICATION NUMBER: US/09/648,386  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 09/371,710  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 50  
SEQ ID NO 48  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer  
US-09-648-386-48

Query Match 47.6%; Score 20; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KYSP 8  
DB 2 KYAP 5

RESULT 15  
US-08-178-570-47  
Sequence 47, Application US/08178570  
Patent No. 5532167  
GENERAL INFORMATION:  
APPLICANT: Lewis C. Cantley  
APPLICANT: Zhou Song Yang  
TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAIVE & COCKFIELD  
STREET: 60 STATE STREET, suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/178,570  
FILING DATE: JANUARY 7, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A., Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-08-178-570-47

Query Match 47.6%; Score 20; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
DB 1 EEEYMP 6

Search completed: January 17, 2002, 12:16:07  
Job time: 112 sec